**Supplementary file 1**

1. **Buffers and solutions**

**Amyloid extraction buffers**

* Homogenization buffer: 10 mM Tris-HCl with 0.25 M sucrose, 3 mM EDTA, 0.1% sodium azide, and protease inhibitor cocktail, pH 7.
* Digestion buffer: collagenase 0.5 mg/mL and DNase I (0.01 mg/mL) in 20 mM Tris pH 8.0 with 2 mM CaCl2, sodium azide (0.01 %).
* Solubilization buffer: 50 mM Tris with 1.3 M sucrose and 1% SDS, pH 8.
* Wash buffer: 50 mM Tris buffer, pH 8.

**Trypsin digestion and peptide cleanup solutions**

* Guanidine hydrochloride buffer: 50 mM ammonium bicarbonate with 6 M guanidine hydrochloride.
* Surfactant solution: 50 mM ammonium bicarbonate with 0.2% MS compatible surfactant.
* C18 spin column equilibration/wash buffer: 5% acetonitrile in HPLC grade water with 0.5% trifluoroacetic acid.
* C18 spin column elution buffer: 70% acetonitrile in HPLC grade water with 0.5% trifluoroacetic acid.

**Mass spectrometry**

* Sample loading buffer: 0.1% formic acid, 2% acetonitrile in MS grade water.

**Other solutions**

* TBST: Tris-buffered saline (150 mM NaCl and 20 mm Tris) containing 0.05% Tween-20.
* Laemmli sample buffer (1x): 2.5 % w/v SDS, 0.0625 M Tris base, 10% glycerol, 5% β-mercaptoethanol, 0.02% w/v bromophenol blue, pH 6.8.
* Congo red solution: Filtered 1% Congo red in 0.5% sodium chloride and 80 % ethanol.

**2. Mass spectrometry parameters (adapted from Hark et al. 2021)**

Set ion transfer tube temperature, default charge state, and cycle time were set to 300 °C, 2, and 3 seconds respectively along with internal mass calibration. Detector type is Orbitrap, with 60 K cycle time, and wide quad isolation with ‘normal’ mass range and scan range ‘300-1500 m/z’. MIPS is set on, included charge states = 2-6 with ‘reject unassigned’. Dynamic exclusion is enabled with n = 1 for 30 s and 45 s exclusion duration at 10 ppm for high and low.

Other important MS parameters are: max injection time 50 ms, AGC target= 200,000, microscans = 1, S-lens RF level = 60, without source fragmentation, and datatype = positive and centroid. Precursor selection decision is most intense with top 20, isolation window = 1.6, scan range = auto normal, first mass = 110, collision energy 30 %, CID, Detector type = ion trap, OT resolution = 30 K, IT scan rate = rapid, max injection time = 75 ms, AGC target = 10,000, Q = 0.25, inject ions for all available parallelizable time.

**3. ProLuCID search parameters for identification of peptides**

**Basic parameters**

Fragmentation activation method: CID

Precursor mass type: Mono

Fragment mass type: Mono

Precursor/peptide mass tolerance: High (50-ppm precursor tolerance)

Precursor mass range: 600-6000

Fragment mass tolerance in ppm: 600

**Enzyme information**

Specificity: Both end

Max. Number internal missed cleavage: Unlimited

Protease name: Trypsin

Residues: KR (Lysine and Arginine)

Cut position: C-terminus

**Static modification**

N-terminus static modification: 0

C-terminus static modification: 0

Amino acid residue specific static modification: 57.02146 C

**Advanced parameters**

Max. # of scans in split spectral files: 4000

Max. number of internal differential modifications: 0

Differential modifications: 0

Metabolic Labelling Search: No

**Advanced ProLuCID search parameters**

Primary score type: Xcorr

Primary score type: Z-score

Are MS/MS spectra deisotoped and decharged: No

Use low fragment ions: No

Multistage Activation Mode: 0 (only non-neutral loss peaks)

Minimum peptide length: 6

Candidate peptide threshold: 600

Peptide N-term diff mods: 0

Peptide C-term diff mods: 0

Calculate PTM localization score: No

**Basic DTASelect 2.0 parameters:**

Minimum number of peptide per protein (-p): 1

Minimum number of tryptic end per peptide (-y): 1

False positive rate (protein): 0.01

Precursor delta mass cutoff (-DM): No

Precursor delta mass shift (-DMS): Do not use

Prefilter noisy PSMs: Do not use

**Advanced DTASelect 2.0 parameters:**

Unique peptides only: No

Unique peptide group: No

Statistics with delta mass (--mass): No

Statistics with modification (--modstat): No

Statistics with tryptic status (--trypstat): Yes

Include subset proteins (-in): No

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